

Automated Medical image segmentation for detection of abnormal masses using Watershed transform and Markov random fields

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Abstract—Research in the segmentation of medical images will strive towards improving the accuracy, precision, and computational speed of segmentation methods, as well as reducing the amount of manual interaction. Accuracy and precision can be improved by incorporating prior information from atlases and by combining discrete and continuous-based segmentation methods. The medical images consists a general framework to segment curvilinear 2D objects The proposed method based on Watershed algorithm is traditionally applied on image domain. Then model uses a Markov chain in scale to model the class labels that form the segmentation, but augments this Markov chain structure by incorporating tree based classifiers to model the transition probabilities between adjacent scales. Experiments with real medical images show that the proposed segmentation framework is efficient.

Index Terms—medical images, marker controlled watershed transform, markov random fields, digital mammograms morphological filtering

I. INTRODUCTION

With the increasing size and number of medical images, the use of computers in facilitating their processing and analysis has become necessary. In particular, computer algorithms for the delineation of anatomical structures and other regions of interest are a key component in assisting and automating specific radiological tasks. These algorithms, called *image segmentation* algorithms, play a vital role in numerous biomedical imaging applications such as the quantification of tissue volumes [1], diagnosis [2], localization of pathology [3], study of anatomical structure [4], treatment planning [5], partial volume correction of functional imaging data [6], and computer integrated surgery [6].

The watershed transform (WT), as explained by Vincent and Soille (1991), is a morphological algorithm usually used for the purpose of segmentation. Considering a gray level image as a topographic map, let us denote by catchment basin associated with a regional minimum of this map, all points whose steepest slope paths reach this minimum.[4,5] watershed line is a closed one-pixel thick crest line which separates every adjacent catchment basins, i.e., regions. Watershed algorithm is a widely used segmentation method. However, in most of cases, the algorithm is based on image domain Markov random field (MRF) modeling itself is not a segmentation method but a statistical model which can be

used within segmentation methods. MRFs model spatial interactions between neighboring or nearby pixels. These local correlations provide a mechanism for modeling a variety of image properties [8]. In medical imaging, they are typically used to take into account the fact that most pixels belong to the same class as their neighboring pixels. In physical terms, this implies that any anatomical structure that consists of only one pixel has a very low probability of occurring under a MRF assumption. MRFs are often incorporated into clustering segmentation algorithms under a Bayesian prior model [7,8]. The segmentation is then obtained by maximizing the a posteriori probability of the segmentation given the image data using iterative methods such as iterated conditional modes [10] or simulated annealing [5,4]. X-ray computed tomography (CT) alleviates some of the difficulties associated with projection radiography and allows for 3-D imaging at resolutions equal to or better than MRI. Soft tissue contrast in CT is not as good as in MRI, but CT remains the modality of choice for imaging bone and bone tumors. Segmentation of bone can be achieved using thresholding and region growing operations [6] as well as more sophisticated methods such as Markov random fields [9], deformable models [13,14], and fuzzy region growing [15]. Once segmented, image renderings are often used to provide detailed visualization of skeletal structure [17]. Segmentation in CT has also been applied to thoracic scans using statistical clustering [16], a combination of region growing and watershed algorithms [18], a combination of region growing and fuzzy logic [15], and deformable models [11 12, 14]. Some methods have been applied specifically for the reconstruction of bronchial trees [18, 19]. CT images have also been used in brain segmentation [15], although MR imaging is presently more common in neuro imaging segmentation applications.

In Section II, we introduce a watershed transformation and a general form of the SMAP estimate derived from our model. The markov random fields is discussed in Section III. Section IV presents the Proposed algorithms developed for our model. Experimental results are discussed in Section V, and Section VI concludes this paper.

II WATERSHED TRANSFORMATION

The watershed constitutes one of the main concepts of Mathematical Morphology. The watershed transform can be

classified as a region-based segmentation approach.

As shown in fig.1 grayscale image can be considered as topographic surface: we regard the intensity of a pixel as altitude of the point. Let us imagine the surface of this relief being immersed in still water, with holes created in local minima. Water fills up the dark areas “the basins” starting at these local minima. Where waters coming from different basins meet we will build dams. When the water level has reached the highest peak in the landscape, the process is stopped. As a result, the landscape is partitioned into regions or basins separated by dams, called watershed lines or simply watersheds[4].

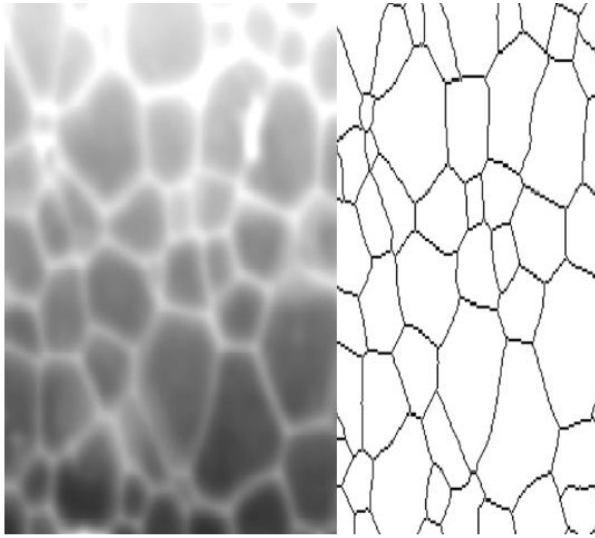


Fig:1 segmentation of an image by watershed transform

A Watershed definitions

A watershed definition for the continuous case can be based on distance functions. Assume that the image f is an element of the space $C(D)$ of real twice continuously differentiable functions on a connected domain D with only isolated critical points. Then the topographical distance between points p and q in D is defined by

$$T_f(p, q) = \inf_{\gamma} \int \|\nabla f(\gamma(s))\| ds$$

where the infimum is over all paths (smooth curves) inside D with $(0) = p$, $(1) = q$. Let have minima $f|_{c(D)} \{m_k\}_{k \in I}$, for some index set I . The catchment basin of a minimum m_i is defined as the set of points which are topographically closer to m_i than to any other regional minimum m_j :

$$CB(m_i) = \{x \in D \mid \forall j \in I \setminus \{i\}: f(m_i) + T_f(x, m_i) < f(m_j) + T_f(x, m_j)\}$$

The watershed of f is the set of points which do not belong to any catchment basin

$$Wshed(f) = D \cap \left(\bigcup_{i \in I} CB(m_i) \right)^c$$

So the watershed transform of f assigns labels to the points of D , such that

- different catchment basins are uniquely labeled, and a
- special label W is assigned to all points of the watershed off.

B. Accuracy of watershed lines

The result should be a close approximation of the continuous case. That is, the digital distances playing a role in the watershed calculation should approximate the Euclidean distance. Chamfer distances are an efficient way to achieve accurate watershed lines. The watershed method in its original form produces a severe over segmentation of the image, i.e., many small basins are produced due to many local minima in the input image. Several approaches exist to avoid this, such as markers or hierarchical watersheds. Parallelization of marker-based watershed algorithms has been studied also.

III. MARKOV RANDOM FIELD

Given an undirected graph $G = (V, E)$, a set of random variables $X = (X_v)_{v \in V}$ indexed by V form a Markov random field with respect to G if they satisfy the following equivalent *A.MARKOV Properties*

Pairwise Markov property: Any two non-adjacent variables are conditionally independent given all other variables:

$$X_u \perp\!\!\!\perp X_v \mid X_{V \setminus \{u, v\}} \quad \text{if } \{u, v\} \notin E$$

Local Markov property: A variable is conditionally independent of all other variables given its neighbours:

$$X_v \perp\!\!\!\perp X_{V \setminus cl(v)} \mid X_{ne(v)}$$

where $ne(v)$ is the set of neighbours of v , and $cl(v) = \{v\} \cup ne(v)$ is the closed neighbourhood of v .

Global Markov property: Any two subsets of variables are conditionally independent given a separating subset:

$$X_A \perp\!\!\!\perp X_B \mid X_S$$

where every path from a node in A to a node in B passes through S .

As the Markov properties of an arbitrary probability distribution can be difficult to establish, a commonly used class of Markov random fields are those that can be factorized according to the cliques of the graph.

Given a set of random variables $X = (X_v)_{v \in V}$, let $P(X=x)$ be the probability of a particular field configuration x in X . That is, $P(X=x)$ is the probability of finding that the random variables X take on the particular value x . Because X is a set, the probability of x should be understood to be taken with respect to a product measure, and can thus be called a *joint density*.

If this joint density can be factorized over the cliques of G :

$$P(X = x) = \prod_{C \in cl(G)} \phi_C(x_C)$$

then X forms a Markov random field with respect to G . Here, $cl(G)$ is the set of cliques of G . The definition is equivalent if only maximal cliques are used. The functions ϕ_C are sometimes referred to as *factor potentials* or *clique potentials*. Note, however, conflicting terminology is in use: the word *potential* is often applied to the logarithm of ϕ_C . This is

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because, in statistical mechanics, $\log(\varphi_c)$ has a direct interpretation as the potential energy of a configuration x_c .

Although some MRFs do not factorize (a simple example can be constructed on a cycle of 4 nodes^[3]), in certain cases they can be shown to be equivalent conditions: if the density is positive.

When such a factorization does exist, it is possible to construct a factor graph for the network..[9]

As we consider in a Bayesian network, one may calculate the conditional distribution of a set of nodes $V' = \{v_1, \dots, v_i\}$ given values to another set of nodes $W' = \{w_1, \dots, w_j\}$ in the Markov random field by summing over all possible assignments to $u \notin V', W'$; this is called exact inference. However, exact inference is a #P-complete problem, and thus computationally intractable in the general case. Approximation techniques such as Markov chain Monte Carlo and loopy belief propagation are often more feasible in practice. Some particular subclasses of MRFs, such as trees (see Chow-Liu tree), have polynomial-time inference algorithms; discovering such subclasses is an active research topic. There are also subclasses of MRFs that permit efficient MAP, or most likely assignment, inference; examples of these include associative networks.[10,11]

IV. PROPOSED WORK

Clique factorization

Although region-based methods are not well suited to segment curvilinear objects, we now propose a framework which relies on a region segmentation algorithm to address this issue.

ALGORITHM

Pre-Processing: From an original image containing curvilinear objects we compute a gray level image where pixel values denote their potential of belonging to these objects. Curvilinear objects are thus located on some parts of the crest lines of this “potential” image.

Morphological Filtering: The filtering step consists in computing an area closing of the potential image and then running the watershed transform. The “closed” potential image has much less minima than the “original” potential image while properly retaining crest lines location. Therefore, the resulting watershed line includes the curvilinear objects. Curve Adjacency Graph. From the watershed line, we build a curve adjacency graph (CAG). A node of this graph represents a shed, that is, a connected part of the watershed line separating two adjacent basins. An edge is drawn between two nodes/sheds if one end of the first shed is connected with a end of the second one through the watershed line. For every node we make the distinction between edges coming from connections to one shed end and those coming from connections to the other shed end. This distinction is symbolized by yellow and blue anchors in the picture above.

Markovian Relaxation Segmenting: curvilinear objects

now turns out to be a graph labeling problem. Upon the graph structure, we define a Markov random field. Let us denote by X the observation field, by Y the result field, by x_s and y_s their respective restriction to a given node s , by Y_V the restriction of Y to the neighborhood of s . The variable y_s has a Boolean realization where 1 means object and 0 means not object. Under the Markovian assumption we have:

The first energy terms, models a priori knowledge about curvilinear objects, and the second energy term, deals with labeling contextual information. Since we have expressed the object segmentation problem as an energy minimization problem, a relaxation process is performed to finally get the segmentation result.

V. RESULTS AND DISCUSSIONS

In medical images diagnosis, x-ray serves as an irreplaceable imaging tool. Polycystic ovary syndrome is the commonest breast tissue disorder in women of reproductive age [1]. The criteria for diagnosing this disease include the ovarian volume and the number of follicles in this volume. Figures as shows an example application of the proposed method in segmenting a mammogram image. As shown in Fig. 2.(a), mammogram images usually contains basins and malignant tumors. Basins is not a cancer tumors where as malignant more strongly effected to get a cancer. Speckle noise is the most prominent artifact images, which blurs the tissue boundary and decreases the signal-to-noise ratio. Morphological filtering is used to suppress the speckle noise. Fig. 2(b) gives the preprocessing. Since the follicles usually have round or elliptical shape, the marker estimation method is also effective in this case. From Fig. 4.(a), we can see that the marker-controlled watershed algorithm successfully identifies each follicle. From the segmented object image, the number and the size of follicles can be estimated easily. The textural feature map (Fig. 3(a) and (b)) generated from fractal dimension analysis appears blurry; however, it provides a correct guide to the markov random field process. The final segmentation is shown in Fig. 4(b). Because of strong artifacts and low resolution, segmentation of ultrasound images is generally difficult. As illustrated in this work, integrated use of intensity, edge, texture, and density information provides an effective method for ultrasound image segmentation

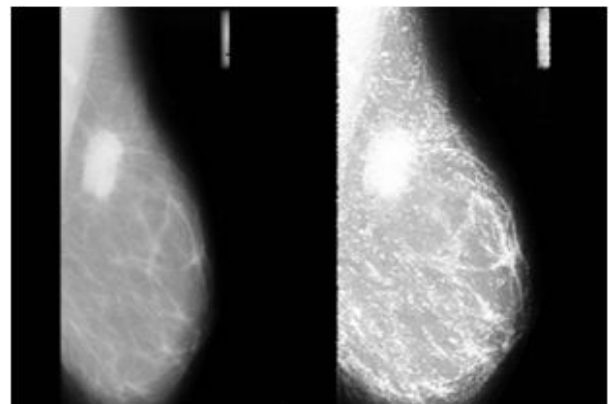


Fig2(A) original mammogram (b) its gradient

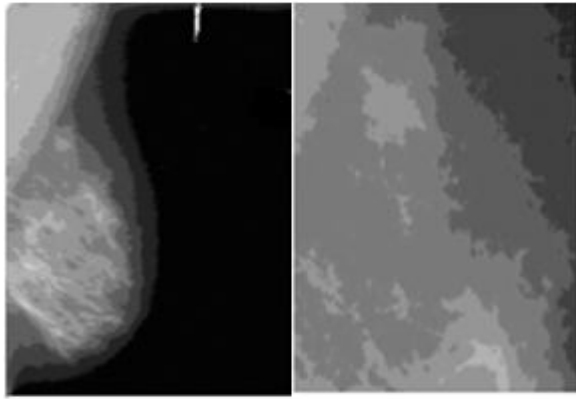


Fig 3(A)mrf fields distributions of image.(b)maligants in the image

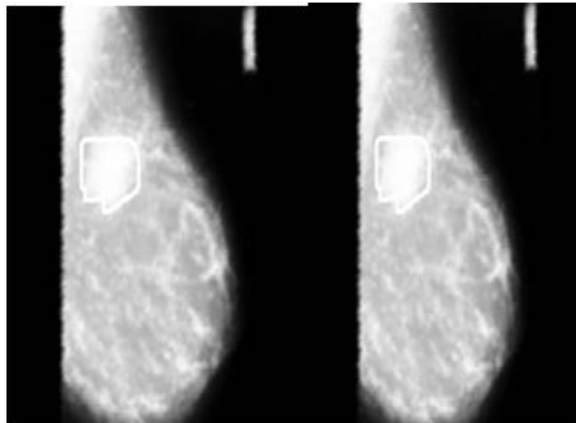


Fig4(a)watershed transformation image and (B)marker final images

VI. CONCLUSIONS

The separation of a image by means Watershed transformations and use of markers has a many advantages. It can provide closed contours for constructions, this property is useful for segmentations process. In this paper, we used a markov random fields in order to segment multispectral images. With combination of watershed and markov random fields offers a efficient results to medical image segmentations. In this proposed we applied on digital mammogram images to detect tumors in breast. This recognition scheme is a global optimization process so it provides robust and reproducible results. Moreover, it is general and can easily be adapted to various image processing fields where the recognition of curvilinear structures is involved. These Segmentation methods will be particularly valuable in areas such as computer integrated surgery, where visualization of the anatomy is a critical component.

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